

**BLAST®** >> **blastn suite** >> results for RID-S4KEEF97015

**Job Title** [Nucleotide Sequence ...](#)  
**RID** [S4KEEF97015](#) Search expires on 09-19 23:31 pm  
**Program** BLASTN  
**Database** nr  
**Query ID** lcl|Query\_137035  
**Description** [None ...](#)  
**Molecule type** dna  
**Query Length** 1092

**Descriptions**

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1858	1858	93%	0.0	99.42%	<a href="#">AK154309.1</a>
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1740	1740	93%	0.0	97.56%	<a href="#">XM_006510253.2</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1740	1882	93%	0.0	97.56%	<a href="#">JN961338.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1740	1882	93%	0.0	97.56%	<a href="#">JN951773.1</a>
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1740	1740	93%	0.0	97.56%	<a href="#">NM_172769.2</a>
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1740	1992	93%	0.0	97.56%	<a href="#">AC160051.2</a>
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	1740	93%	0.0	97.56%	<a href="#">AK077670.1</a>
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	1740	93%	0.0	97.56%	<a href="#">AK043825.1</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1576	1576	93%	0.0	94.63%	<a href="#">XM_029481771.1</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1576	1576	93%	0.0	94.63%	<a href="#">XM_021172472.2</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1576	1576	93%	0.0	94.63%	<a href="#">XM_021172471.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1103	1103	91%	0.0	87.55%	<a href="#">XM_021207205.2</a>
Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds	979	979	49%	0.0	99.44%	<a href="#">AB016248.1</a>
Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	977	48%	0.0	100.00%	<a href="#">BC024132.1</a>
PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	749	749	91%	0.0	81.24%	<a href="#">XM_017595406.1</a>
Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	749	749	91%	0.0	81.24%	<a href="#">NM_053642.2</a>
Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	792	56%	0.0	90.04%	<a href="#">AC122333.2</a>
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	699	57%	0.0	87.84%	<a href="#">XM_021207206.2</a>
Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	678	48%	0.0	89.80%	<a href="#">NR_136927.1</a>
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	678	48%	0.0	89.80%	<a href="#">AK052921.1</a>
PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	579	49%	1e-160	87.25%	<a href="#">XM_029547953.1</a>
PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	678	77%	6e-114	79.62%	<a href="#">XM_005069403.3</a>
Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	407	47%	6e-109	81.46%	<a href="#">AB052846.1</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	396	396	53%	1e-105	79.44%	<a href="#">XM_007651891.3</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	396	396	53%	1e-105	79.44%	<a href="#">XM_003511371.4</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	392	392	53%	2e-104	79.30%	<a href="#">XM_027411877.1</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	392	392	53%	2e-104	79.30%	<a href="#">XM_027411876.1</a>
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence	311	311	16%	5e-80	97.79%	<a href="#">AK165139.1</a>
Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730048E03 product:unclassifiable, full insert sequence	292	292	16%	2e-74	96.61%	<a href="#">AK050439.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Cd3eap:tm1a(KOMP)Wtsi; transgenic	185	303	11%	3e-42	93.65%	<a href="#">JN957866.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ercc1:tm1a(KOMP)Wtsi tm2a(KOMP)Wtsi; transgenic	185	394	11%	3e-42	93.65%	<a href="#">JN955142.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Cd3eap:tm1e(KOMP)Wtsi; transgenic	185	303	11%	3e-42	93.65%	<a href="#">JN949926.1</a>
Mus musculus CD3E antigen, epsilon polypeptide associated protein (Cd3eap), mRNA	185	185	11%	3e-42	93.65%	<a href="#">NM_145822.2</a>
Mus musculus chromosome 7, clone RP23-457C1, complete sequence	185	1735	14%	3e-42	93.65%	<a href="#">AC118017.15</a>
Mus musculus BAC clone RP23-152A3 from chromosome 9, complete sequence	185	1367	15%	3e-42	88.12%	<a href="#">AC159821.2</a>
Mus musculus BAC clone RP23-85B15 from chromosome 7, complete sequence	185	1346	13%	3e-42	93.65%	<a href="#">AC148988.5</a>
Mus musculus BAC clone RP23-135K11 from chromosome 8, complete sequence	183	2499	15%	1e-41	86.78%	<a href="#">AC163625.5</a>
Mus musculus strain C57BL/6J chromosome 8 clone rp23-340n2, complete sequence	183	1760	14%	1e-41	86.78%	<a href="#">AC093451.25</a>
Mus musculus chromosome 12, clone RP24-276C17, complete sequence	182	1209	15%	4e-41	92.91%	<a href="#">AC115037.16</a>
Mus musculus BAC clone RP24-140F3 from 12, complete sequence	182	921	11%	4e-41	92.91%	<a href="#">AC117240.4</a>
Mus musculus BAC clone RP23-322K1 from chromosome 14, complete sequence	180	1311	15%	1e-40	92.31%	<a href="#">AC125180.6</a>
Mus musculus BAC clone RP23-240E9 from chromosome 9, complete sequence	180	728	14%	1e-40	87.50%	<a href="#">AC160392.2</a>
Mus musculus CD3E antigen, epsilon polypeptide associated protein, mRNA (cDNA clone MGC:78047 IMAGE:6478245), complete cds	180	180	11%	1e-40	92.80%	<a href="#">BC071199.1</a>
Mus musculus BAC clone RP23-358C4 from chromosome 9, complete sequence	178	178	14%	5e-40	86.39%	<a href="#">AC183268.4</a>
Mus musculus BAC clone RP23-408I18 from chromosome 9, complete sequence	178	178	14%	5e-40	86.39%	<a href="#">AC153009.4</a>
Mouse DNA sequence from clone RP23-253E9 on chromosome 11, complete sequence	178	3465	15%	5e-40	86.39%	<a href="#">AL591113.14</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X8, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_030252585.1</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X7, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_030252584.1</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X6, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_017319548.2</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X5, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_006501389.4</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X4, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_017319547.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X3, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_017319546.1</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X2, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_006501386.3</a>
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X1, mRNA	176	176	13%	2e-39	88.16%	<a href="#">XM_006501385.3</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb22:tm1a(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	<a href="#">JN963878.1</a>
Mus musculus targeted deletion, lacZ-tagged mutant allele Sf3b4:tm1(KOMP)Ucd; transgenic	176	292	14%	2e-39	88.16%	<a href="#">JN960976.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb26:tm1a(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	<a href="#">JN959925.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele 9130017N09Rik:tm2e(EUCOMM)Wtsi tm1e(EUCOMM)Wtsi; transgenic	176	534	11%	2e-39	92.13%	<a href="#">JN958274.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele 9130017N09Rik:tm2a(EUCOMM)Wtsi; transgenic	176	534	11%	2e-39	92.13%	<a href="#">JN958273.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb26:tm1e(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	<a href="#">JN956718.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Otud7b:tm1a(EUCOMM)Wtsi; transgenic	176	343	13%	2e-39	88.16%	<a href="#">JN952505.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb22:tm1e(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	<a href="#">JN948829.1</a>
Mus musculus BAC clone RP23-13B8 from chromosome 10, complete sequence	176	2625	11%	2e-39	92.13%	<a href="#">AC151846.3</a>
Mus musculus chromosome 15, clone RP23-195124, complete sequence	176	503	11%	2e-39	92.19%	<a href="#">AC161812.3</a>
Mus musculus chromosome 1, clone RP24-400M20, complete sequence	176	817	11%	2e-39	92.13%	<a href="#">AC116853.12</a>
Mus musculus BAC clone RP24-389C22 from chromosome 10, complete sequence	176	1627	11%	2e-39	92.13%	<a href="#">AC124407.4</a>
Mus musculus chromosome 15, clone RP24-366J14, complete sequence	176	853	11%	2e-39	92.19%	<a href="#">AC163018.3</a>
Mus musculus chromosome 2 clone RP23-286D16, complete sequence	176	685	14%	2e-39	87.12%	<a href="#">AC019153.13</a>
Mouse DNA sequence from clone RP23-332C5 on chromosome 11, complete sequence	176	290	14%	2e-39	87.20%	<a href="#">AL645738.14</a>
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 1, mRNA	176	176	13%	2e-39	88.16%	<a href="#">NM_001025613.1</a>
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 2, mRNA	176	176	13%	2e-39	88.16%	<a href="#">NM_001025614.1</a>
Mus musculus BAC clone RP23-138K22 from 9, complete sequence	176	1679	11%	2e-39	92.13%	<a href="#">AC140409.3</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus BAC clone RP24-201C14 from 3, complete sequence	176	739	14%	2e-39	88.16%	<a href="#">AC125099.3</a>
Mouse DNA sequence from clone RP23-453K8 on chromosome 2, complete sequence	176	499	15%	2e-39	87.42%	<a href="#">AL844517.6</a>
Mouse DNA sequence from clone RP23-188D9 on chromosome 2, complete sequence	176	685	14%	2e-39	87.50%	<a href="#">BX004793.12</a>
Mus musculus strain C57BL/6J chromosome 3 clone rp23-261m19, complete sequence	176	803	14%	2e-39	88.16%	<a href="#">AC092094.19</a>
Mouse DNA sequence from clone RP23-391H10 on chromosome 2, complete sequence	176	1193	15%	2e-39	92.19%	<a href="#">AL805959.11</a>
Mouse DNA sequence from clone RP23-120N11 on chromosome 4, complete sequence	176	1727	14%	2e-39	92.13%	<a href="#">AL683890.7</a>
Mouse DNA sequence from clone RP23-129N7 on chromosome 5, complete sequence	176	1345	11%	2e-39	91.54%	<a href="#">AL513345.20</a>
Mus musculus FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1), transcript variant 2, mRNA	174	174	15%	6e-39	85.23%	<a href="#">NM_001290430.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ftsj1:tm1e(EUCOMM)Wtsi; transgenic	174	433	15%	6e-39	85.23%	<a href="#">JN961376.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Fbxo17:tm1e(EUCOMM)Wtsi; transgenic	174	613	14%	6e-39	87.04%	<a href="#">JN957410.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnd1:tm1a(EUCOMM)Wtsi; transgenic	174	303	15%	6e-39	85.71%	<a href="#">JN954778.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Mical2:tm1e(KOMP)Wtsi; transgenic	174	288	10%	6e-39	92.68%	<a href="#">JN954776.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Hnrnpu:tm1e(EUCOMM)Wtsi; transgenic	174	174	14%	6e-39	86.31%	<a href="#">JN953467.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Mical2:tm1a(KOMP)Wtsi; transgenic	174	288	10%	6e-39	92.68%	<a href="#">JN950802.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Hnrnpu:tm1a(EUCOMM)Wtsi; transgenic	174	174	14%	6e-39	86.31%	<a href="#">JN949506.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fbxo17:tm1a(EUCOMM)Wtsi; transgenic	174	613	14%	6e-39	87.04%	<a href="#">JN949490.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnd1:tm1e(EUCOMM)Wtsi; transgenic	174	303	15%	6e-39	85.71%	<a href="#">JN947814.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ywhaq:tm1e(EUCOMM)Hmgu; transgenic	174	418	14%	6e-39	90.91%	<a href="#">JN947747.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ywhaq:tm1a(EUCOMM)Hmgu; transgenic	174	418	14%	6e-39	90.91%	<a href="#">JN947251.1</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ftsj1:tm1a(EUCOMM)Wtsi; transgenic	174	433	15%	6e-39	85.23%	<a href="#">JN945613.1</a>
Mus musculus chromosome 1, clone RP24-252K15, complete sequence	174	1034	14%	6e-39	86.67%	<a href="#">AC166710.7</a>
Mus musculus BAC clone RP23-27C10 from chromosome 1, complete sequence	174	1055	14%	6e-39	86.67%	<a href="#">AC125377.5</a>
Mus musculus BAC clone RP23-264L8 from chromosome 14, complete sequence	174	844	11%	6e-39	92.06%	<a href="#">AC158983.2</a>
Mus musculus BAC clone RP23-168E11 from chromosome 5, complete sequence	174	1239	13%	6e-39	92.68%	<a href="#">AC130221.4</a>
Mus musculus BAC clone RP24-505G5 from chromosome 7, complete sequence	174	376	14%	6e-39	88.51%	<a href="#">AC125372.4</a>
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832403P19 product:DSCAM-interacting protein 1 homolog [Mus musculus], full insert sequence	174	174	14%	6e-39	86.50%	<a href="#">AK161178.1</a>
Mus musculus BAC clone RP24-490B17 from chromosome 17, complete sequence	174	174	11%	6e-39	90.91%	<a href="#">AC154796.2</a>
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630055M22 product:Ftsj homolog (E. coli), full insert sequence	174	174	15%	6e-39	85.23%	<a href="#">AK036313.1</a>

## Graphic Summary

Distribution of the top 420 Blast Hits on 100 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature

Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence  
Sequence ID: **AK154309.1** Length: 2251 Number of Matches: 1  
Range 1: 1101 to 2127

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

	1858 bits(1006)	0.0()	1021/1027(99%)	5/1027(0%)	Plus/Plus	
Query	71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT				130
Sbjct	1101	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT				1160
Query	131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC				190
Sbjct	1161	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC				1220
Query	191	AGGAACAACCTTGTC'TTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT				250
Sbjct	1221	AGGAACAACCTTGTC'TTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT				1280
Query	251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT				310
Sbjct	1281	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT				1340
Query	311	GCATACTCATTAAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA				370
Sbjct	1341	GCATACTCATTAAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA				1400
Query	371	ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA				430
Sbjct	1401	ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA				1460
Query	431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG				490
Sbjct	1461	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG				1520
Query	491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT				550
Sbjct	1521	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT				1580
Query	551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTA'ttttttttAAA				610
Sbjct	1581	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTA'ttttttttAAA				1640
Query	611	TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG				670
Sbjct	1641	TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG				1700
Query	671	AGTGTCA'tttttttttctttc-----tttttttttttttttttttgg'ttttttAAGACAG				725
Sbjct	1701	AGTGTCA'tttttttttctttc-----tttttttttttttttttttgg'ttttttAAGACAG				1760
Query	726	GGTTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTC				785
Sbjct	1761	GGTTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTC				1820
Query	786	AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGT				845
Sbjct	1821	AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGT				1880
Query	846	GTGTCATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTA				905
Sbjct	1881	GTGTCATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTA				1940
Query	906	TAAACTTGTGGCACCCAGTGACATC'tttttttAATCAAGTGGACACACTTTTGATGTATT				965
Sbjct	1941	TAAACTTGTGGCACCCAGTGACATC'tttttttAATCAAGTGGACACACTTTTGATGTATT				2000
Query	966	TCTCAGTTACAAAGCTGACT'tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTA				1025
Sbjct	2001	TCTCAGTTACAAAGCTGACT'tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTA				2060
Query	1026	CCTAAGGTACACTTTAGACCTCATCTTCTATTCTTCCCTCTCTTCTGCAAATGAACAAA				1085
Sbjct	2061	CCTAAGGTACACTTTAGACCTCATCTTCTATTCTTCCCTCTCTTCTGCAAATGAACAAA				2120
Query	1086	ACAAAAC 1092				
Sbjct	2121	ACAAAAC 2127				

PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA

Sequence ID: **XM\_006510253.2** Length: 4826 Number of Matches: 1

Range 1: 1146 to 2158

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query	71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT			130



```

Sbjct 1146 GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT 1205
Query 131 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC 190
Sbjct 1206 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC 1265
Query 191 AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 250
Sbjct 1266 AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 1325
Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 310
Sbjct 1326 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 1385
Query 311 GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 370
Sbjct 1386 GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 1445
Query 371 ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGTGTTGGGA 430
Sbjct 1446 ACCCTAAGATGAAGATGGTCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGTGTTGGGA 1505
Query 431 GTTGACAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG 490
Sbjct 1506 GTTGACAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG 1565
Query 491 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT 550
Sbjct 1566 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT 1625
Query 551 TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA 610
Sbjct 1626 TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA 1685
Query 611 TGTCAGCTCTTCCATAATTCACTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 670
Sbjct 1686 TGTCAGCTCTTCCATAATTCACTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 1743
Query 671 AGTGTCAtttttttttctttcttttttttttttttttttggttttttAAGACAGGGTTT 730
Sbjct 1744 AGTGTCATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGGTTT 1794
Query 731 CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 790
Sbjct 1795 CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 1854
Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGTGTGTC 850
Sbjct 1855 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGAAAGTGTGTC 1914
Query 851 ATTTAAACCCTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 910
Sbjct 1915 ATTTAAACCCTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 1974
Query 911 TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTCTCA 970
Sbjct 1975 TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTCTCA 2034
Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 1029
Sbjct 2035 GTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 2094
Query 1030 AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 1088
Sbjct 2095 AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 2154
Query 1089 AAAC 1092
Sbjct 2155 AAAC 2158

```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic  
Sequence ID: **JN961338.1** Length: 38137 Number of Matches: 2  
Range 1: 26029 to 27041

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	130			
Sbjct 26029	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	26088			
Query 131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 26089	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	26148			

```

Query 191      AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 250
Sbjct 26149    AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 26208

Query 251      AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 310
Sbjct 26209    AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 26268

Query 311      GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 370
Sbjct 26269    GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 26328

Query 371      ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA 430
Sbjct 26329    ACCCTAACGATGAAGATGGTCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA 26388

Query 431      GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG 490
Sbjct 26389    GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG 26448

Query 491      TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT 550
Sbjct 26449    TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT 26508

Query 551      TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAAttttttttAAA 610
Sbjct 26509    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA 26568

Query 611      TGTACGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTGGTG 670
Sbjct 26569    TGTACGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 26626

Query 671      AGTGTCAAttttttttctttcttttttttttttttttttttggtttttAAGACAGGGTTT 730
Sbjct 26627    AGTGTCAATTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTC AAGACAGGGTTT 26677

Query 731      CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 790
Sbjct 26678    CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 26737

Query 791      TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGATGTGTGTC 850
Sbjct 26738    TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGAAGTGTGTC 26797

Query 851      ATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 910
Sbjct 26798    ATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 26857

Query 911      TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 970
Sbjct 26858    TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 26917

Query 971      GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 1029
Sbjct 26918    GTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 26977

Query 1030     AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 1088
Sbjct 26978    AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 27037

Query 1089     AAAC 1092
Sbjct 27038     AAAC 27041

```

Range 2: 37078 to 37200

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	7e-29()	108/123(88%)	4/123(3%)	Plus/Plus	
Query 682	tttttctttcttttttttttttttttttttggtttttAAGACAGGGTTTCTCTGTGTAGC	741			
Sbjct 37078	TTTTTGTTTTTTGTTTTTTTGTGTTTTGTTTTGTTTTTAAGACAGGGTTTCTCTGTGTAGC	37137			
Query 742	CCTGGCTGTCTGGAACCT--T--GTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT	797			
Sbjct 37138	CCTGGCTGTCTGGAACCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT	37197			
Query 798	GCC 800				
Sbjct 37198	GCC 37200				

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic

Sequence ID: **JN951773.1** Length: 38097 Number of Matches: 2

Range 1: 25989 to 27001

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	130			
Sbjct 25989	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	26048			
Query 131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 26049	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	26108			
Query 191	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250			
Sbjct 26109	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	26168			
Query 251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	310			
Sbjct 26169	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	26228			
Query 311	GCATACTCATTAAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370			
Sbjct 26229	GCATACTCATTAAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	26288			
Query 371	ACCCTAAAGATGAAGATGTTCTGTCCCCGGAGCGCTGGCTCCACCGCAGTGCTGGGGA	430			
Sbjct 26289	ACCCTAACGATGAAGATGGTCTGTCCCCGGAGCGCTGGCTCCACCGAAGTGCTGGGGA	26348			
Query 431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490			
Sbjct 26349	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG	26408			
Query 491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATGTACTTCCTATACAGAGGCACCT	550			
Sbjct 26409	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATGTACTTCCTATACAGAGGCACCT	26468			
Query 551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAatTTTTTTAAA	610			
Sbjct 26469	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTAAA	26528			
Query 611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670			
Sbjct 26529	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG	26586			
Query 671	AGTGTCAatTTTTTTTTctttctTTTTTTTTTTTTTTTTTTTTTggtTTTTAAGACAGGGTTT	730			
Sbjct 26587	AGTGTCATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGGTTT	26637			
Query 731	CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790			
Sbjct 26638	CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	26697			
Query 791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGATGTGTGTC	850			
Sbjct 26698	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGAAGTGTGTC	26757			
Query 851	ATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910			
Sbjct 26758	ATTTAAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	26817			
Query 911	TTGTGGCACCCAGTGACATCtTTTTTTAATCAAGTGACACACTTTTGATGTATTTCTCA	970			
Sbjct 26818	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGACACACTTTTGATGTATTTCTCA	26877			
Query 971	GTTACAAAGCTGAC-tTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029			
Sbjct 26878	GTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	26937			
Query 1030	AGGTACAC-TTTAGACCTCATCTTCTATTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088			
Sbjct 26938	AGGTACACTTTTAAACCTCATCTTCTATTCTTCCCTCTCTTCTGCAAATGAACAAAACA	26997			
Query 1089	AAAC 1092				
Sbjct 26998	AAAC 27001				

Range 2: 37038 to 37160

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	7e-29()	108/123(88%)	4/123(3%)	Plus/Plus	

Query	682	tttttctttcttttttttttttttttttttggttttttAAGACAGGGTTTCTCTGTGTAGC	741
Sbjct	37038	TTTTTGTTTTTTGTTTTTTTGTGTTTTGTTTTTAAGACAGGGTTTCTCTGTGTAGC	37097
Query	742	CCTGGCTGTCCTGGAACCT--T--GTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT	797
Sbjct	37098	CCTGGCTGTCCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT	37157
Query	798	GCC	800
Sbjct	37158	GCC	37160

## Mus musculus sterol-C5-desaturase (Sc5d), mRNA

Sequence ID: **NM\_172769.2** Length: 2249 Number of Matches: 1

Range 1: 1154 to 2166

Score		Expect	Identities	Gaps	Strand	Frame
1740 bits(942)		0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query	71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT CATGCTGAGGGATGGTCTCTGACAGT				130
Sbjct	1154	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT CATGCTGAGGGATGGTCTCTGACAGT				1213
Query	131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGTTAATTGTCCGACATTGGTCC				190
Sbjct	1214	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGTTAATTGTCCGACATTGGTCC				1273
Query	191	AGGAACAAC TTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT				250
Sbjct	1274	AGGAACAAC TTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT				1333
Query	251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT				310
Sbjct	1334	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT				1393
Query	311	GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA				370
Sbjct	1394	GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA				1453
Query	371	ACCCTAAGATGAAGATGTTCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA				430
Sbjct	1454	ACCCTAACGATGAAGATGGTCTGTCCGGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA				1513
Query	431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG				490
Sbjct	1514	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG				1573
Query	491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT				550
Sbjct	1574	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT				1633
Query	551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA				610
Sbjct	1634	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAA				1693
Query	611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG				670
Sbjct	1694	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG				1751
Query	671	AGTGTCAAttttttttttctttcttttttttttttttttttggttttttAAGACAGGGTTT				730
Sbjct	1752	AGTGTCATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGGTTT				1802
Query	731	CTCTGTGTAGCCCTGGCTGTCTGGAAC TCTGTAGACTGGGCTGGCCTCGAACTCAGAGA				790
Sbjct	1803	CTCTGTGTAGCCCTGGCTGTCTGGAAC TCTGTAGACTGGGCTGGCCTCGAACTCAGAGA				1862
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCAC TGCCAGCTTGATGTGTGTC				850
Sbjct	1863	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCAC TGCCAGCTTGAAGTGTGTC				1922
Query	851	ATTTAAACCACTGTTTAATAAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC				910
Sbjct	1923	ATTTAAACCACTGTTTAATAAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC				1982
Query	911	TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA				970
Sbjct	1983	TTGTGGCACCCAGTGACATCTTTTTTAAATCAAGTGGACACACTTTTGATGTATTTCTCA				2042
Query	971	GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA				1029
Sbjct	2043	GTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG				2102
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA				1088

```

Sbjct  2103  AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA  2162
Query   1089  AAAC   1092
Sbjct  2163  AAAC   2166

```

Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence

Sequence ID: **AC160051.2** Length: 199433 Number of Matches: 3

Range 1: 34694 to 35706

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCC TGACAGT	130			
Sbjct 34694	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCC TGACAGT	34753			
Query 131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 34754	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	34813			
Query 191	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250			
Sbjct 34814	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	34873			
Query 251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	310			
Sbjct 34874	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	34933			
Query 311	GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370			
Sbjct 34934	GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	34993			
Query 371	ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	430			
Sbjct 34994	ACCCTAACGATGAAGATGGTCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA	35053			
Query 431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490			
Sbjct 35054	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	35113			
Query 491	TGGATAGGATTTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT	550			
Sbjct 35114	TGGATAGGATTTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT	35173			
Query 551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTA ttttttttAAA	610			
Sbjct 35174	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTA ttttttttAAA	35233			
Query 611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670			
Sbjct 35234	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG	35291			
Query 671	AGTGTCA tttttttttctttcttttttttttttttttttttgg ttttttAAGACAGGGTTT	730			
Sbjct 35292	AGTGTCA tttttttttctttcttttttttttttttttttttgg ttttttAAGACAGGGTTT	35342			
Query 731	CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790			
Sbjct 35343	CTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	35402			
Query 791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGATGTGTGTC	850			
Sbjct 35403	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGAAGTGTGTC	35462			
Query 851	ATTTAAAACCACTGTTTAATAACCCACAGACATGAATCTGGATAATGCTAGGTATAAAC	910			
Sbjct 35463	ATTTAAAACCACTGTTTAATAACCCACAGACATGAATCTGGATAATGCTAGGTATAAAC	35522			
Query 911	TTGTGGCACCCAGTGACATC ttttttttAATCAAGTGGACACACTTTTGATGTATTCTCA	970			
Sbjct 35523	TTGTGGCACCCAGTGACATC ttttttttAATCAAGTGGACACACTTTTGATGTATTCTCA	35582			
Query 971	GTTACAAAGCTGAC- ttttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029			
Sbjct 35583	GTTACAAAGCTGAC ttttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	35642			
Query 1030	AGGTACAC- TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088			
Sbjct 35643	AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	35702			
Query 1089	AAAC   1092				

Sbjct 35703 AAAC 35706

Range 2: 45743 to 45865

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	7e-29()	108/123(88%)	4/123(3%)	Plus/Plus	
Query 682	tttttctttcttttttttttttttttttttggttttttAAGACAGGGTTTCTCTGTGTAGC	741			
Sbjct 45743	TTTTTGTTTTTTGTTTTTTGTGTTTTGTTTTTAAGACAGGGTTTCTCTGTGTAGC	45802			
Query 742	CCTGGCTGTCCTGGAAGCTC--T--GTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT	797			
Sbjct 45803	CCTGGCTGTCCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT	45862			
Query 798	GCC 800				
Sbjct 45863	GCC 45865				

Range 3: 139035 to 139134

Score	Expect	Identities	Gaps	Strand	Frame
110 bits(59)	2e-19()	87/100(87%)	4/100(4%)	Plus/Minus	
Query 705	ttttttggttttttAAGACAGGGTTTCTCTGTGTAGCCCTGGCTGTCTTGGAAGCTC----	760			
Sbjct 139134	TTTGTGGCTTTTTGAGACAGGGTTTCTCTGTGTAGCCCTGGCTGTCTTGGAAGCTCACTC	139075			
Query 761	TGTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCTGCC 800				
Sbjct 139074	TGTAGACCAGGCTGGCCTTGAAGCTCAGAAATCCACCTGCC 139035				

Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence

Sequence ID: **AK077670.1** Length: 2207 Number of Matches: 1

Range 1: 1112 to 2124

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	130			
Sbjct 1112	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	1171			
Query 131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 1172	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	1231			
Query 191	AGGAACAACCTTGCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250			
Sbjct 1232	AGGAACAACCTTGCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	1291			
Query 251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	310			
Sbjct 1292	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	1351			
Query 311	GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370			
Sbjct 1352	GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	1411			
Query 371	ACCCTAAAGATGAAGATGTTCTGTCCTCCCGGAGCGGCTGGCTCCACCGCAGTGCCTGGGGA	430			
Sbjct 1412	ACCCTAACGATGAAGATGGTCCTGTCCTCCCGGAGCGGCTGGCTCCACCGAAGTGCCTGGGGA	1471			
Query 431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490			
Sbjct 1472	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG	1531			
Query 491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT	550			
Sbjct 1532	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCATACAGAGGCACCT	1591			
Query 551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAattttttttAAA	610			
Sbjct 1592	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA	1651			

```

Query 611  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 670
Sbjct 1652  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 1709

Query 671  AGTGTCAtttttttttctttcttttttttttttttttttttggttttttAAGACAGGGTTT 730
Sbjct 1710  AGTGTCATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGGTTT 1760

Query 731  CTCTGTGTAGCCCTGGCTGTCCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 790
Sbjct 1761  CTCTGTGTAGCCCTGGCTGTCCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 1820

Query 791  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC 850
Sbjct 1821  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC 1880

Query 851  ATTTAAACCCTGTTTAATAACCTTACAGACATGAATCTGGATAATGCTAGGTATAAAC 910
Sbjct 1881  ATTTAAACCCTGTTTAATAACCTTACAGACATGAATCTGGATAATGCTAGGTATAAAC 1940

Query 911  TTGTGGCACCCAGTGACATCtttttttAATCAAGTGACACACTTTTGATGTATTTCTCA 970
Sbjct 1941  TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGACACACTTTTGATGTATTTCTCA 2000

Query 971  GTTACAAAGCTGAC-ttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 1029
Sbjct 2001  GTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 2060

Query 1030  AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 1088
Sbjct 2061  AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA 2120

Query 1089  AAAC 1092
Sbjct 2121  AAAC 2124

```

Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence

Sequence ID: **AK043825.1** Length: 2209 Number of Matches: 1

Range 1: 1113 to 2125

Score	Expect	Identities	Gaps	Strand	Frame
1740 bits(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	130			
Sbjct 1113	GTGGTGCCATTGGAATGTCAGCATGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	1172			
Query 131	AAACAGCGGGAAGACACCGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 1173	AAACAGCGGGAAGACACCGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	1232			
Query 191	AGGAACAACCTTGCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250			
Sbjct 1233	AGGAACAACCTTGCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	1292			
Query 251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	310			
Sbjct 1293	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	1352			
Query 311	GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370			
Sbjct 1353	GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	1412			
Query 371	ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGTGGGGA	430			
Sbjct 1413	ACCCTAACGATGAAGATGGTCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGTGGGGA	1472			
Query 431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490			
Sbjct 1473	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	1532			
Query 491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	550			
Sbjct 1533	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	1592			
Query 551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA	610			
Sbjct 1593	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA	1652			
Query 611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670			

Sbjct	1653	TGTCAGCTCTTCCATAAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG	1710
Query	671	AGTGTCA <del>tttttttttctttcttttttttttttttttttttttgggtttttt</del> AAGACAGGGTTT	730
Sbjct	1711	AGTGTCA <del>TTTTTTTTTCTTT-TTTC-----TTTTTTTGGT</del> TTTTCAAGACAGGGTTT	1761
Query	731	CTCTGTGTAGCCCTGGCTGTCTGGAAC <del>TCTGTAGACTGGGCTGGCCTCGAACTCAGAGA</del>	790
Sbjct	1762	CTCTGTGTAGCCCTGGCTGTCTGGAAC <del>TCTGTAGACTGGGCTGGCCTCGAACTCAGAGA</del>	1821
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCAC <del>TGCCAGCTTGATGTGTGTC</del>	850
Sbjct	1822	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCAC <del>TGCCAGCTTGAAGTGTGTC</del>	1881
Query	851	ATTTAA <del>AACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC</del>	910
Sbjct	1882	ATTTAA <del>AACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC</del>	1941
Query	911	TTGTGGCACC <del>CAGTGACATCttttttt</del> AATCAAGTGGACACACTTTTGATGTATTCTCA	970
Sbjct	1942	TTGTGGCACC <del>CAGTGACATCTTTTTT</del> AATCAAGTGGACACACTTTTGATGTATTCTCA	2001
Query	971	GTTACAAAGCTGAC- <del>ttttttt</del> AATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2002	GTTACAAAGCTGAC <del>TTTTTTT</del> AATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	2061
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088
Sbjct	2062	AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	2121
Query	1089	AAAC	1092
Sbjct	2122	AAAC	2125

PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA

Sequence ID: **XM\_029481771.1** Length: 2336 Number of Matches: 1

Range 1: 1184 to 2198

Score		Expect	Identities	Gaps	Strand	Frame
1576 bits(853)		0.0()	970/1025(95%)	13/1025(1%)	Plus/Plus	
Query	71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	CATGCTGAGGGATGGTCTGACAGT			130
Sbjct	1184	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	CATGCTGAGGGATGGTCTGACAGT			1243
Query	131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTG	TGGTTAATTGTCCGACATTGGTCC			190
Sbjct	1244	AAACAGCGGGAAGGCACCGGGAGCATTGTAATCTCTTG	TGGTTAATTGTCCGACATTGGTCC			1303
Query	191	AGGAACAATTGTCTTTTCAGCCGGCTGACCTGCAGCCTGT	TACAGCTCTGAAGCATCTTT			250
Sbjct	1304	AGGAACAATTGTCTTTTCAGCCGGCTGACCTGCAGCCTGT	TACAGCTCCGAAGCATCTTT			1363
Query	251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGT	GTCTTTTGCCTTAGTCCAT			310
Sbjct	1364	AAATACGATAGAAAATAAGCTACTCAAGAACTGGTCTGCGT	CTTTTGCCTTAATCCAT			1423
Query	311	GCATACTCATTAAGG	aaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA			370
Sbjct	1424	GCATACTCATTAAGG	AAAAAAAAAGTACCATTGTGCTTAGCGCTACTGAGACTAACCAGGAA			1483
Query	371	ACCCTAAAGATGAAGATGTTCTGTCCCCGGAGCGGCTGGCT	CCACCGCAGTGCTGGGGA			430
Sbjct	1484	ACCCTAAAGATGAAGATGCTCCCGTTCCCGGAGTGCCGGCTGC	ACAGCAGTGCTGGGGA			1543
Query	431	GTTGCAGGACTTCATTCAATAGGAATATCAGTCCAAGCAGGCT	GATACGTGAGTGGCAG			490
Sbjct	1544	GCTGCAGGACTTCATTCAAGATAGGAGTATCAGTCCAAGCAGGCT	GATACGTGAGTGGCAG			1603
Query	491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTT	CCTATACAGAGGCACCT			550
Sbjct	1604	CGGGTAGGATTTGCTTAATGGCTGATGTAATAAGATTGGACTT	CCTGTACGTAGGCACCT			1663
Query	551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAAATAAAT	TGGTAttttttttAAA			610
Sbjct	1664	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAAATAAAT	TGGTATTTTTTTTAA			1723
Query	611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACT	GAAGATCTCTTGGTG			670
Sbjct	1724	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGACTATTTAACT	GAAGA--TCTTGGTG			1781
Query	671	AGTGTCA	tttttttttctttcttttttttttttttttttggttttttAAGACAGGGTTT			730
Sbjct	1782	AGTGTCA	TATTATT---TTTCTTTTTC--TTTTTTTTTTTTTGGTTTTTCAAGACAGGGTTT			1836



```

Query 731 CTCTGTGTAGCCCTGGCTGTCCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 790
Sbjct 1837 CTCTGTGTAGCCCTGGCTGTCCTAGAACTCTGTAGACTGGGCTGGTCTCGAACTCAGAGA 1896

Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCAGCTTGATGTGTGTC 850
Sbjct 1897 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTTACCACC--T-CCCAGCTTGATGTGTGTC 1953

Query 851 ATTTAAACCCTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 910
Sbjct 1954 ATTTAAACCCTGTTTAATAATCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 2013

Query 911 TTGTGGCACCCAGTGACATC-ttttttAATCAAGTGACACACTTTGTATGTTTCTC 969
Sbjct 2014 TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGACACACTTTGTATGTTTCTC 2073

Query 970 AGTTACAAAGCTGACttttttAATGAAGGGAATAATGGCAAGTACTTAAATCTACCTA 1029
Sbjct 2074 AGTTACAAAGCTGACTTTTTTCATGAAGGGAATAATGGCAAGTACTCAAATCTACCTG 2133

Query 1030 AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAA-CAAAAC 1087
Sbjct 2134 AGGTACACTTTTACACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATAAAACAAAC 2193

Query 1088 AAAAC 1092
Sbjct 2194 AAAAC 2198

```

PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA

Sequence ID: **XM\_021172472.2** Length: 2297 Number of Matches: 1

Range 1: 1145 to 2159

Score	Expect	Identities	Gaps	Strand	Frame
1576 bits(853)	0.0()	970/1025(95%)	13/1025(1%)	Plus/Plus	
Query 71	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCTATGCTGAGGGATGGTCCTGACAGT	130			
Sbjct 1145	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCTATGCTGAGGGATGGTCCTGACAGT	1204			
Query 131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190			
Sbjct 1205	AAACAGCGGGAAGGACCCGGGAGCATTGTAATCTCTTGGTTAATTGTCCGACATTGGTCC	1264			
Query 191	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250			
Sbjct 1265	AGGAACAATTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCCGAAGCATCTTT	1324			
Query 251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	310			
Sbjct 1325	AAATACGATAGAAAATAAGCTACTCAAGAACTGGTCTGCGTCCTTTTGCCTTAATCCAT	1384			
Query 311	GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370			
Sbjct 1385	GCATACTCATTAAGGAAAAAAGTACCATTGTGCTTAGCGCTACTGAGACTAACCAGGAA	1444			
Query 371	ACCCTAAAGATGAAGATGTTCTGTCCTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	430			
Sbjct 1445	ACCCTAAAGATGAAGATGCTCCCGTTCCTCCGAGTGGCCGGCTGCACAGCAGTGCTGGGGA	1504			
Query 431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490			
Sbjct 1505	GCTGCAGGACTTCATTCAAGATAGGATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	1564			
Query 491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	550			
Sbjct 1565	CGGGTAGGATTTGCTTAATGGCTGATGTAATAAGATTGGACTTCCTGTACGTAGGCACCT	1624			
Query 551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAtttttttAAA	610			
Sbjct 1625	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA	1684			
Query 611	TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670			
Sbjct 1685	TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGACTATTTAACTGAAGA--TCTTGGTG	1742			
Query 671	AGTGTCAtttttttttctttcttttttttttttttttttgggttttttAAGACAGGGTTT	730			
Sbjct 1743	AGTGTCAATTTATTT---TTTCTTTTTC--TTTTTTTTTTTGGTTTTTCAAGACAGGGTTT	1797			
Query 731	CTCTGTGTAGCCCTGGCTGTCCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790			
Sbjct 1798	CTCTGTGTAGCCCTGGCTGTCCTAGAACTCTGTAGACTGGGCTGGTCTCGAACTCAGAGA	1857			

9/18/2019NCBI Blast:Nucleotide Sequence

Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCTGCCAGCTTGATGTGTGTC	850
Sbjct	1858	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTTACACCACC--T-CCCAGCTTGATGTGTGTC	1914
Query	851	ATTTAAACCACTGTTTAATAACCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1915	ATTTAAACCACTGTTTAATAATCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	1974
Query	911	TTGTGGCACCCAGTGACATC-ttttttAATCAAGTGGACACACTTTTGATGTATTTCTC	969
Sbjct	1975	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTC	2034
Query	970	AGTTACAAAGCTGACttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2035	AGTTACAAAGCTGACTTTTTTTCATGAAGGGAATAATTGCCAAGTACTCAAATCTACCTG	2094
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAA-CAAAAC	1087
Sbjct	2095	AGGTACACTTTTACACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATAAAACAAAAC	2154
Query	1088	AAAAC	1092
Sbjct	2155	AAAAC	2159

Taxonomy

Reports

Lineage

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">Muroidea</a>	<a href="#">rodents</a>		<a href="#">101</a>	
<a href="#">.Murinae</a>	<a href="#">rodents</a>		<a href="#">96</a>	
<a href="#">..Mus</a>	<a href="#">rodents</a>		<a href="#">92</a>	
<a href="#">...Mus</a>	<a href="#">rodents</a>		<a href="#">89</a>	
<a href="#">....Mus musculus</a>	<a href="#">rodents</a>	1858	<a href="#">86</a>	<a href="#">Mus musculus hits</a>
<a href="#">....Mus caroli</a>	<a href="#">rodents</a>	1576	<a href="#">3</a>	<a href="#">Mus caroli hits</a>
<a href="#">...Mus pahari</a>	<a href="#">rodents</a>	1103	<a href="#">3</a>	<a href="#">Mus pahari hits</a>
<a href="#">..Rattus norvegicus</a>	<a href="#">rodents</a>	749	<a href="#">4</a>	<a href="#">Rattus norvegicus hits</a>
<a href="#">.Mesocricetus auratus</a>	<a href="#">rodents</a>	424	<a href="#">1</a>	<a href="#">Mesocricetus auratus hits</a>
<a href="#">.Cricetulus griseus</a>	<a href="#">rodents</a>	396	<a href="#">4</a>	<a href="#">Cricetulus griseus hits</a>

Organism

Description	Score	E value	Accession
Mus musculus (house mouse) [rodents ]			
<a href="#">Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence</a>	1858	0.0	<a href="#">AK154309</a>
<a href="#">PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1740	0.0	<a href="#">XM_006510253</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgü; transgenic</a>	1740	0.0	<a href="#">JN961338</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgü; transgenic</a>	1740	0.0	<a href="#">JN951773</a>
<a href="#">Mus musculus sterol-C5-desaturase (Sc5d), mRNA</a>	1740	0.0	<a href="#">NM_172769</a>
<a href="#">Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence</a>	1740	0.0	<a href="#">AC160051</a>

Description	Score	E value	Accession
<a href="#">Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	1740	0.0	<a href="#">AK077670</a>
<a href="#">Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	1740	0.0	<a href="#">AK043825</a>
<a href="#">Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds</a>	979	0.0	<a href="#">AB016248</a>
<a href="#">Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds</a>	977	0.0	<a href="#">BC024132</a>
<a href="#">Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence</a>	702	0.0	<a href="#">AC122333</a>
<a href="#">Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA</a>	678	0.0	<a href="#">NR_136927</a>
<a href="#">Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence</a>	678	0.0	<a href="#">AK052921</a>
<a href="#">Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	311	5e-80	<a href="#">AK165139</a>
<a href="#">Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730048E03 product:unclassifiable, full insert sequence</a>	292	2e-74	<a href="#">AK050439</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Cd3eap:tm1a(KOMP)Wtsi; transgenic</a>	185	3e-42	<a href="#">JN957866</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ercc1:tm1a(KOMP)Wtsi tm2a(KOMP)Wtsi; transgenic</a>	185	3e-42	<a href="#">JN955142</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Cd3eap:tm1e(KOMP)Wtsi; transgenic</a>	185	3e-42	<a href="#">JN949926</a>
<a href="#">Mus musculus CD3E antigen, epsilon polypeptide associated protein (Cd3eap), mRNA</a>	185	3e-42	<a href="#">NM_145822</a>
<a href="#">Mus musculus chromosome 7, clone RP23-457C1, complete sequence</a>	185	3e-42	<a href="#">AC118017</a>
<a href="#">Mus musculus BAC clone RP23-152A3 from chromosome 9, complete sequence</a>	185	3e-42	<a href="#">AC159821</a>
<a href="#">Mus musculus BAC clone RP23-85B15 from chromosome 7, complete sequence</a>	185	3e-42	<a href="#">AC148988</a>
<a href="#">Mus musculus BAC clone RP23-135K11 from chromosome 8, complete sequence</a>	183	1e-41	<a href="#">AC163625</a>
<a href="#">Mus musculus strain C57BL/6J chromosome 8 clone rp23-340n2, complete sequence</a>	183	1e-41	<a href="#">AC093451</a>
<a href="#">Mus musculus chromosome 12, clone RP24-276C17, complete sequence</a>	182	4e-41	<a href="#">AC115037</a>
<a href="#">Mus musculus BAC clone RP24-140F3 from 12, complete sequence</a>	182	4e-41	<a href="#">AC117240</a>
<a href="#">Mus musculus BAC clone RP23-322K1 from chromosome 14, complete sequence</a>	180	1e-40	<a href="#">AC125180</a>
<a href="#">Mus musculus BAC clone RP23-240E9 from chromosome 9, complete sequence</a>	180	1e-40	<a href="#">AC160392</a>
<a href="#">Mus musculus CD3E antigen, epsilon polypeptide associated protein, mRNA (cDNA clone MGC:78047 IMAGE:6478245), complete cds</a>	180	1e-40	<a href="#">BC071199</a>
<a href="#">Mus musculus BAC clone RP23-358C4 from chromosome 9, complete sequence</a>	178	5e-40	<a href="#">AC183268</a>
<a href="#">Mus musculus BAC clone RP23-408I18 from chromosome 9, complete sequence</a>	178	5e-40	<a href="#">AC153009</a>
<a href="#">Mouse DNA sequence from clone RP23-253E9 on chromosome 11, complete sequence</a>	178	5e-40	<a href="#">AL591113</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X8, mRNA</a>	176	2e-39	<a href="#">XM_030252585</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X7, mRNA</a>	176	2e-39	<a href="#">XM_030252584</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X6, mRNA</a>	176	2e-39	<a href="#">XM_017319548</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X5, mRNA</a>	176	2e-39	<a href="#">XM_006501389</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X4, mRNA</a>	176	2e-39	<a href="#">XM_017319547</a>

Description	Score	E value	Accession
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X3, mRNA</a>	176	2e-39	<a href="#">XM_017319546</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X2, mRNA</a>	176	2e-39	<a href="#">XM_006501386</a>
<a href="#">PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X1, mRNA</a>	176	2e-39	<a href="#">XM_006501385</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb22:tm1a(KOMP)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN963878</a>
<a href="#">Mus musculus targeted deletion, lacZ-tagged mutant allele Sf3b4:tm1(KOMP)Ucd; transgenic</a>	176	2e-39	<a href="#">JN960976</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb26:tm1a(KOMP)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN959925</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele 9130017N09Rik:tm2e(EUCOMM)Wtsi tm1e(EUCOMM)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN958274</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele 9130017N09Rik:tm2a(EUCOMM)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN958273</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb26:tm1e(KOMP)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN956718</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Otud7b:tm1a(EUCOMM)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN952505</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb22:tm1e(KOMP)Wtsi; transgenic</a>	176	2e-39	<a href="#">JN948829</a>
<a href="#">Mus musculus BAC clone RP23-13B8 from chromosome 10, complete sequence</a>	176	2e-39	<a href="#">AC151846</a>
<a href="#">Mus musculus chromosome 15, clone RP23-195I24, complete sequence</a>	176	2e-39	<a href="#">AC161812</a>
<a href="#">Mus musculus chromosome 1, clone RP24-400M20, complete sequence</a>	176	2e-39	<a href="#">AC116853</a>
<a href="#">Mus musculus BAC clone RP24-389C22 from chromosome 10, complete sequence</a>	176	2e-39	<a href="#">AC124407</a>
<a href="#">Mus musculus chromosome 15, clone RP24-366J14, complete sequence</a>	176	2e-39	<a href="#">AC163018</a>
<a href="#">Mus musculus chromosome 2 clone RP23-286D16, complete sequence</a>	176	2e-39	<a href="#">AC019153</a>
<a href="#">Mouse DNA sequence from clone RP23-332C5 on chromosome 11, complete sequence</a>	176	2e-39	<a href="#">AL645738</a>
<a href="#">Mus musculus OTU domain containing 7B (Otud7b), transcript variant 1, mRNA</a>	176	2e-39	<a href="#">NM_001025613</a>
<a href="#">Mus musculus OTU domain containing 7B (Otud7b), transcript variant 2, mRNA</a>	176	2e-39	<a href="#">NM_001025614</a>
<a href="#">Mus musculus BAC clone RP23-138K22 from 9, complete sequence</a>	176	2e-39	<a href="#">AC140409</a>
<a href="#">Mus musculus BAC clone RP24-201C14 from 3, complete sequence</a>	176	2e-39	<a href="#">AC125099</a>
<a href="#">Mouse DNA sequence from clone RP23-453K8 on chromosome 2, complete sequence</a>	176	2e-39	<a href="#">AL844517</a>
<a href="#">Mouse DNA sequence from clone RP23-188D9 on chromosome 2, complete sequence</a>	176	2e-39	<a href="#">BX004793</a>
<a href="#">Mus musculus strain C57BL/6J chromosome 3 clone rp23-261m19, complete sequence</a>	176	2e-39	<a href="#">AC092094</a>
<a href="#">Mouse DNA sequence from clone RP23-391H10 on chromosome 2, complete sequence</a>	176	2e-39	<a href="#">AL805959</a>
<a href="#">Mouse DNA sequence from clone RP23-120N11 on chromosome 4, complete sequence</a>	176	2e-39	<a href="#">AL683890</a>
<a href="#">Mouse DNA sequence from clone RP23-129N7 on chromosome 5, complete sequence</a>	176	2e-39	<a href="#">AL513345</a>
<a href="#">Mus musculus FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1), transcript variant 2, mRNA</a>	174	6e-39	<a href="#">NM_001290430</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ftsj1:tm1e(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN961376</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Fbxo17:tm1e(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN957410</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnd1:tm1a(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN954778</a>

Description	Score	E value	Accession
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Micall2:tm1e(KOMP)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN954776</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Hnrnpu:tm1e(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN953467</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Micall2:tm1a(KOMP)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN950802</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Hnrnpu:tm1a(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN949506</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fbxo17:tm1a(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN949490</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnd1:tm1e(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN947814</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ywhaq:tm1e(EUCOMM)Hmgu; transgenic</a>	174	6e-39	<a href="#">JN947747</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ywhaq:tm1a(EUCOMM)Hmgu; transgenic</a>	174	6e-39	<a href="#">JN947251</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ftsj1:tm1a(EUCOMM)Wtsi; transgenic</a>	174	6e-39	<a href="#">JN945613</a>
<a href="#">Mus musculus chromosome 1, clone RP24-252K15, complete sequence</a>	174	6e-39	<a href="#">AC166710</a>
<a href="#">Mus musculus BAC clone RP23-27C10 from chromosome 1, complete sequence</a>	174	6e-39	<a href="#">AC125377</a>
<a href="#">Mus musculus BAC clone RP23-264L8 from chromosome 14, complete sequence</a>	174	6e-39	<a href="#">AC158983</a>
<a href="#">Mus musculus BAC clone RP23-168E11 from chromosome 5, complete sequence</a>	174	6e-39	<a href="#">AC130221</a>
<a href="#">Mus musculus BAC clone RP24-505G5 from chromosome 7, complete sequence</a>	174	6e-39	<a href="#">AC125372</a>
<a href="#">Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832403P19 product:DSCAM-interacting protein 1 homolog [Mus musculus], full insert sequence</a>	174	6e-39	<a href="#">AK161178</a>
<a href="#">Mus musculus BAC clone RP24-490B17 from chromosome 17, complete sequence</a>	174	6e-39	<a href="#">AC154796</a>
<a href="#">Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630055M22 product:Ftsj homolog (E. coli), full insert sequence</a>	174	6e-39	<a href="#">AK036313</a>
Mus caroli (Ryukyu mouse) [rodents ]			
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA</a>	1576	0.0	<a href="#">XM_029481771</a>
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	1576	0.0	<a href="#">XM_021172472</a>
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1576	0.0	<a href="#">XM_021172471</a>
Mus pahari (shrew mouse) [rodents ]			
<a href="#">PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1103	0.0	<a href="#">XM_021207205</a>
<a href="#">PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	699	0.0	<a href="#">XM_021207206</a>
<a href="#">PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA</a>	579	1e-160	<a href="#">XM_029547953</a>
Rattus norvegicus (Norway rat) [rodents ]			
<a href="#">PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	749	0.0	<a href="#">XM_017595406</a>
<a href="#">Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA</a>	749	0.0	<a href="#">NM_053642</a>
<a href="#">Rattus norvegicus sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like, mRNA (cDNA clone MGC:93101 IMAGE:7131154), complete cds</a>	749	0.0	<a href="#">BC081704</a>
<a href="#">Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds</a>	407	6e-109	<a href="#">AB052846</a>
Mesocricetus auratus (golden hamster) [rodents ]			
<a href="#">PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA</a>	424	6e-114	<a href="#">XM_005069403</a>
Cricetulus griseus (Chinese hamster) [rodents ]			
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	396	1e-105	<a href="#">XM_007651891</a>

Description	Score	E value	Accession
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	396	1e-105	<a href="#">XM_003511371</a>
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	392	2e-104	<a href="#">XM_027411877</a>
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	392	2e-104	<a href="#">XM_027411876</a>

## ◦ Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
<a href="#">Muroidea</a>	<a href="#">101</a>	6	
. <a href="#">Murinae</a>	<a href="#">96</a>	4	
.. <a href="#">Mus</a>	<a href="#">92</a>	3	
... <a href="#">Mus</a>	<a href="#">89</a>	2	
.... <a href="#">Mus musculus</a>	<a href="#">86</a>	1	<a href="#">Mus musculus hits</a>
.... <a href="#">Mus caroli</a>	<a href="#">3</a>	1	<a href="#">Mus caroli hits</a>
... <a href="#">Mus pahari</a>	<a href="#">3</a>	1	<a href="#">Mus pahari hits</a>
.. <a href="#">Rattus norvegicus</a>	<a href="#">4</a>	1	<a href="#">Rattus norvegicus hits</a>
. <a href="#">Cricetinae</a>	<a href="#">5</a>	2	
.. <a href="#">Mesocricetus auratus</a>	<a href="#">1</a>	1	<a href="#">Mesocricetus auratus hits</a>
.. <a href="#">Cricetulus griseus</a>	<a href="#">4</a>	1	<a href="#">Cricetulus griseus hits</a>

[Top](#)